

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/746,919DATE: 03/22/2001
TIME: 23:32:22

INPUT SET: S36555.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

ENTERED

1
2
3 (1) General Information:
4 (i) APPLICANT: Johnson, Howard M.
5 Pontzer, Carol H.
6
7 (ii) TITLE OF INVENTION: Interferon Tau Compositions and
8 Methods of Use
9
10 (iii) NUMBER OF SEQUENCES: 44
11
12 (iv) CORRESPONDENCE ADDRESS:
13 (A) ADDRESSEE: Dehlinger & Associates
14 (B) STREET: 350 Cambridge Ave., Suite 250
15 (C) CITY: Palo Alto
16 (D) STATE: CA
17 (E) COUNTRY: USA
18 (F) ZIP: 94306
19
20 (v) COMPUTER READABLE FORM:
21 (A) MEDIUM TYPE: Floppy disk
22 (B) COMPUTER: IBM PC compatible
23 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
24 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
25
26 (vi) CURRENT APPLICATION DATA:
27 (A) APPLICATION NUMBER: 09/746,919
28 (B) FILING DATE:
29 (C) CLASSIFICATION:
30
31 (vii) PRIOR APPLICATION DATA:
32 (A) APPLICATION NUMBER: 09/045,467
33 (B) FILING DATE:
34
35 (vii) PRIOR APPLICATION DATA:
36 (A) APPLICATION NUMBER: US 08/438,753
37 (B) FILING DATE: 10-MAY-1995
38
39
40 (vii) PRIOR APPLICATION DATA:
41 (A) APPLICATION NUMBER: US 08/139,891
42 (B) FILING DATE: 19-OCT-1993
43
44 (vii) PRIOR APPLICATION DATA:
45 (A) APPLICATION NUMBER: US 07/847,741
46 (B) FILING DATE: 09-MAR-1992

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47
48 (vii) PRIOR APPLICATION DATA:
49 (A) APPLICATION NUMBER: US 07/318,050
50 (B) FILING DATE: 02-MAR-1989
51
52 (vii) PRIOR APPLICATION DATA:
53 (A) APPLICATION NUMBER: US 07/969,890
54 (B) FILING DATE: 30-OCT-1992
55
56 (viii) ATTORNEY/AGENT INFORMATION:
57 (A) NAME: Dehlinger, Peter J.
58 (B) REGISTRATION NUMBER: 28,006
59 (C) REFERENCE/DOCKET NUMBER: 5600-0001.36
60
61 (ix) TELECOMMUNICATION INFORMATION:
62 (A) TELEPHONE: 650-324-0880
63 (B) TELEFAX: 650-324-0960
64
65 (2) INFORMATION FOR SEQ ID NO:1:
66
67 (i) SEQUENCE CHARACTERISTICS:
68 (A) LENGTH: 516 base pairs
69 (B) TYPE: nucleic acid
70 (C) STRANDEDNESS: double
71 (D) TOPOLOGY: circular
72
73 (ii) MOLECULE TYPE: DNA
74
75 (iii) HYPOTHETICAL: NO
76
77 (iv) ANTI-SENSE: NO
78
79 (vi) ORIGINAL SOURCE:
80 (A) ORGANISM: Ovis aries
81 (B) STRAIN: Domestic
82 (D) DEVELOPMENTAL STAGE: Blastula (blastocyst)
83 (F) TISSUE TYPE: Trophectoderm
84 (G) CELL TYPE: Mononuclear trophectoderm cells
85
86 (vii) IMMEDIATE SOURCE:
87 (B) CLONE: oTP-1a
88
89 (viii) POSITION IN GENOME:
90 (C) UNITS: bp
91
92 (ix) FEATURE:
93 (A) NAME/KEY: CDS
94 (B) LOCATION: 1..516
95 (x) PUBLICATION INFORMATION:
96 (A) AUTHORS: Ott, Troy L
97 Van Heeke, Gino
98 Johnson, Howard M
99 Bazer, Fuller W

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100 (B) TITLE: Cloning and Expression in Saccharomyces
101 cerevisiae of a Synthetic Gene for the Type I
102 Trophoblast Interferon Ovine Trophoblast
103 Protein-1: Purification and Antiviral Activity
104 (C) JOURNAL: J. Interferon Res.
105 (D) VOLUME: 11
106 (F) PAGES: 357-364
107 (G) DATE: 1991
108 (K) RELEVANT RESIDUES IN SEQ ID NO:1: FROM 1 TO 516
109
110

111 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
112

113	TGC TAC CTG TCG CGA AAA CTG ATG CTG GAC GCT CGA GAA AAT TTA AAA	48
114	Cys Tyr Leu Ser Arg Lys Leu Met Leu Asp Ala Arg Glu Asn Leu Lys	
115	1 5 10 15	
116		
117	CTG CTG GAC CGT ATG AAT CGA TTG TCT CCG CAC AGC TGC CTG CAA GAC	96
118	Leu Leu Asp Arg Met Asn Arg Leu Ser Pro His Ser Cys Leu Gln Asp	
119	20 25 30	
120		
121	CGG AAA GAC TTC GGT CTG CCG CAG GAA ATG GTT GAA GGT GAC CAA CTG	144
122	Arg Lys Asp Phe Gly Leu Pro Gln Glu Met Val Glu Gly Asp Gln Leu	
123	35 40 45	
124		
125	CAA AAA GAC CAA GCT TTC CCG GTA CTG TAT GAA ATG CTG CAG CAG TCT	192
126	Gln Lys Asp Gln Ala Phe Pro Val Leu Tyr Glu Met Leu Gln Gln Ser	
127	50 55 60	
128		
129	TTC AAC CTG TTC TAC ACT GAA CAT TCT TCG GCC GCT TGG GAC ACT ACT	240
130	Phe Asn Leu Phe Tyr Thr Glu His Ser Ser Ala Ala Trp Asp Thr Thr	
131	65 70 75 80	
132		
133	CTT CTA GAA CAA CTG TGC ACT GGT CTG CAA CAG CAA CTG GAC CAT CTG	288
134	Leu Leu Glu Gln Leu Cys Thr Gly Leu Gln Gln Gln Leu Asp His Leu	
135	85 90 95	
136		
137	GAC ACT TGC CGT GGC CAG GTT ATG GGT GAA GAA GAC TCT GAA CTG GGT	336
138	Asp Thr Cys Arg Gly Gln Val Met Gly Glu Glu Asp Ser Glu Leu Gly	
139	100 105 110	
140		
141	AAC ATG GAT CCG ATC GTT ACT GTT AAA AAA TAT TTC CAG GGT ATC TAC	384
142	Asn Met Asp Pro Ile Val Thr Val Lys Lys Tyr Phe Gln Gly Ile Tyr	
143	115 120 125	
144		
145	GAC TAC CTG CAG GAA AAA GGT TAC TCT GAC TGC GCT TGG GAA ATC GTA	432
146	Asp Tyr Leu Gln Glu Lys Gly Tyr Ser Asp Cys Ala Trp Glu Ile Val	
147	130 135 140	
148		
149	CGC GTT GAA ATG ATG CGG GCC CTG ACT GTG TCG ACT ACT CTG CAA AAA	480
150	Arg Val Glu Met Met Arg Ala Leu Thr Val Ser Thr Thr Leu Gln Lys	
151	145 150 155 160	
152		

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516

153 CGG TTA ACT AAA ATG GGT GGT GAC CTG AAT TCT CCG
154 Arg Leu Thr Lys Met Gly Gly Asp Leu Asn Ser Pro
155 165 170
156

157 (2) INFORMATION FOR SEQ ID NO:2:
158

159 (i) SEQUENCE CHARACTERISTICS:

160 (A) LENGTH: 172 amino acids

161 (B) TYPE: amino acid

162 (D) TOPOLOGY: linear
163

164 (ii) MOLECULE TYPE: protein
165

166 (vi) ORIGINAL SOURCE:

167 (C) INDIVIDUAL ISOLATE: amino acid sequence of a mature
168 OvIFNtau protein
169

170 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
171

172 Cys Tyr Leu Ser Arg Lys Leu Met Leu Asp Ala Arg Glu Asn Leu Lys
173 1 5 10 15
174
175 Leu Leu Asp Arg Met Asn Arg Leu Ser Pro His Ser Cys Leu Gln Asp
176 20 25 30
177
178 Arg Lys Asp Phe Gly Leu Pro Gln Glu Met Val Glu Gly Asp Gln Leu
179 35 40 45
180
181 Gln Lys Asp Gln Ala Phe Pro Val Leu Tyr Glu Met Leu Gln Gln Ser
182 50 55 60
183
184 Phe Asn Leu Phe Tyr Thr Glu His Ser Ser Ala Ala Trp Asp Thr Thr
185 65 70 75 80
186
187 Leu Leu Glu Gln Leu Cys Thr Gly Leu Gln Gln Gln Leu Asp His Leu
188 85 90 95
189
190 Asp Thr Cys Arg Gly Gln Val Met Gly Glu Glu Asp Ser Glu Leu Gly
191 100 105 110
192
193 Asn Met Asp Pro Ile Val Thr Val Lys Lys Tyr Phe Gln Gly Ile Tyr
194 115 120 125
195
196 Asp Tyr Leu Gln Glu Lys Gly Tyr Ser Asp Cys Ala Trp Glu Ile Val
197 130 135 140
198
199 Arg Val Glu Met Met Arg Ala Leu Thr Val Ser Thr Thr Leu Gln Lys
200 145 150 155 160
201
202 Arg Leu Thr Lys Met Gly Gly Asp Leu Asn Ser Pro
203 165 170
204
205

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206 (2) INFORMATION FOR SEQ ID NO:3:

207

208 (i) SEQUENCE CHARACTERISTICS:

209 (A) LENGTH: 516 base pairs

210 (B) TYPE: nucleic acid

211 (C) STRANDEDNESS: single

212 (D) TOPOLOGY: linear

213

214 (ii) MOLECULE TYPE: cDNA

215

216 (vi) ORIGINAL SOURCE:

217 (C) INDIVIDUAL ISOLATE: synthetic nucleotide sequence encoding
218 a mature human interferon-tau protein, HuIFNtau1.
219

220 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

221

222 TGTGACTTGT CTCAAAACCA CGTTTTGGTT GGTAGAAAGA ACTTAAGACT ACTAGACGAA 60

223

224 ATGAGACGTC TATCTCCACG CTTCTGTCTA CAAGACAGAA AGGACTTCGC TTTGCCTCAG 120

225

226 GAAATGGTTG AAGGTGGCCA ACTACAAGAA GCTCAAGCGA TATCTGTTTT GCACGAAATG 180

227

228 TTGCAACAAA GCTTCAACTT GTTCCACACC GAACACTCTT CGGCCGCTTG GGACACCACC 240

229

230 TTGTTGGAAC AGCTCAGAAC CGGTTTGCAC CAACAATTGG ACAACTTGGG TGCATGTTTG 300

231

232 GGTCAAGTTA TGGGTGAAGA AGACTCTGCT CTCGGGAGAA CCGGTCCAAC GCTAGCTTTG 360

233

234 AAGAGATACT TCCAAGGTAT CCACGTTTAC TTGAAGGAAA AGGGTTACTC TGACTGTGCT 420

235

236 TGGGAAACCG TCGCTCTAGA AATCATGCGT AGCTTCTCTT CTTTGATCAG CTTGCAAGAA 480

237

238 AGATTACGTA TGATGGACGG TGAATTGTCT AGCCCA 516

239

240

241 (2) INFORMATION FOR SEQ ID NO:4:

242

243 (i) SEQUENCE CHARACTERISTICS:

244 (A) LENGTH: 172 amino acids

245 (B) TYPE: amino acid

246 (C) STRANDEDNESS: single

247 (D) TOPOLOGY: linear

248

249 (ii) MOLECULE TYPE: protein

250

251 (vi) ORIGINAL SOURCE:

252 (C) INDIVIDUAL ISOLATE: amino acid sequence for a mature
253 HuIFNtau protein, HuIFNtau1.
254

255 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

256

257 Cys Asp Leu Ser Gln Asn His Val Leu Val Gly Arg Lys Asn Leu Arg

258 1 5 10 15

PAGE: 1

SEQUENCE VERIFICATION REPORT
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